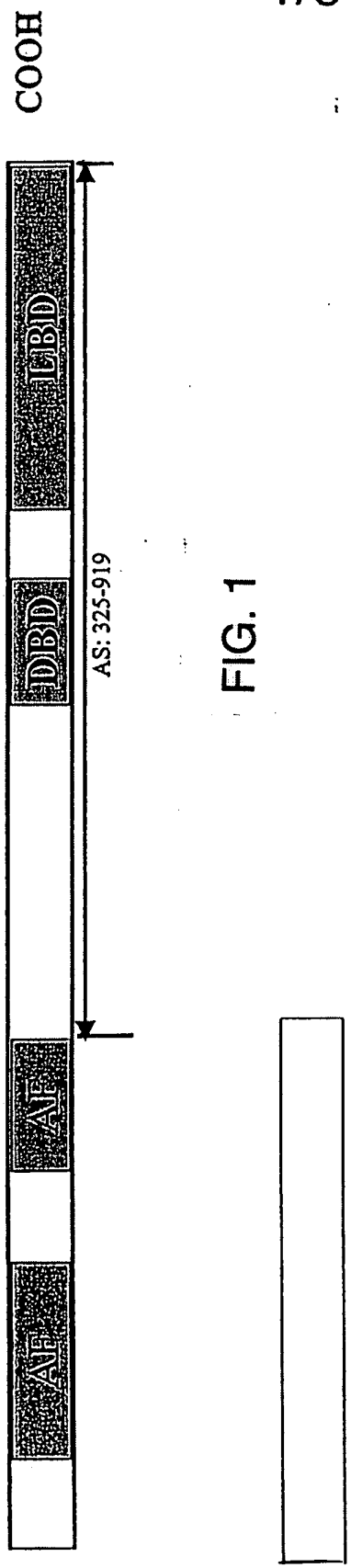


FIG. 1

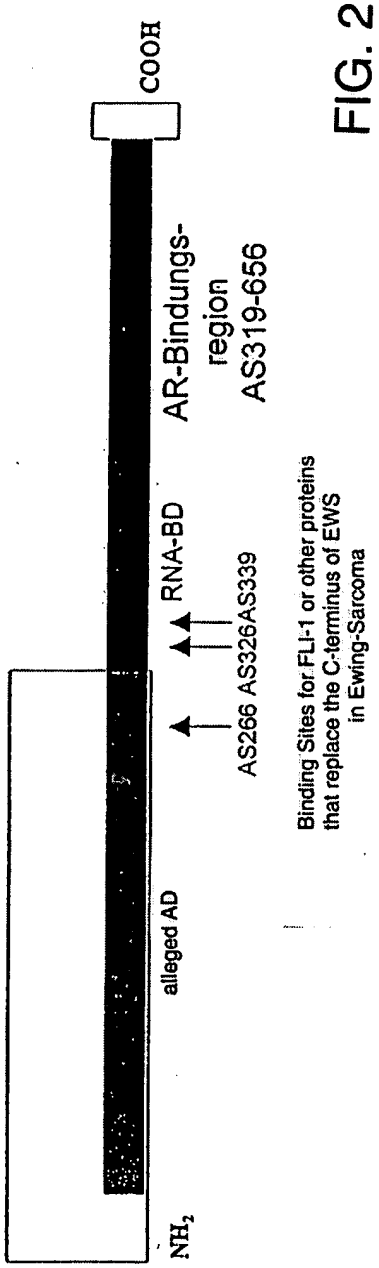
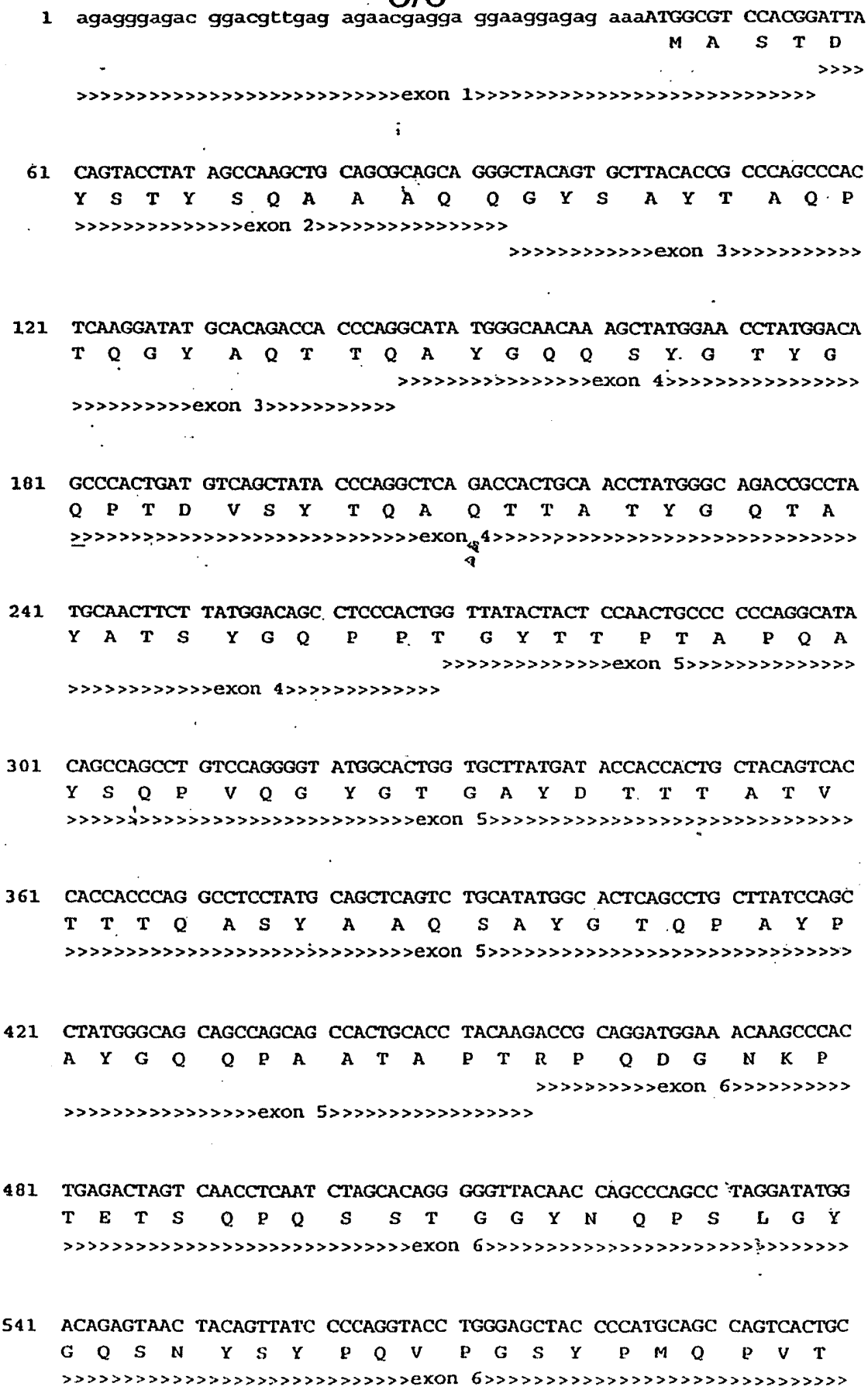

COOH
AR-Bindungs-
region
AS319-656
RNA-BD
AS326AS339
AS266
alleged AD
NH2
Binding Sites for FLI-1 or other proteins
that replace the C-terminus of EWS
in Ewing-Sarcoma

FIG. 2

FIG. 3


1 agagggagac ggacgttgag agaacgagga ggaaggagag aaaATGGCGT CCACGGATTA
M A S T D
>>>>
>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 1>>>>>>>>>>>>>>>>>>>>>>>>>>>>
61 CAGTACCTAT AGCCAAGCTG CAGCGCAGCA GGGCTACAGT GCTTACACCG CCCAGCCCAC
Y S T Y S Q A A A Q Q G Y S A Y T A Q P
>>>>>>>>>>>>>>>exon 2>>>>>>>>>>>>>>>>>
>>>>>>>>>>>>>exon 3>>>>>>>>>>>
121 TCAAGGATAT GCACAGACCA CCCAGGCATA TGGGCAACAA AGCTATGGAA CCTATGGACA
T Q G Y A Q T T Q A Y G Q Q S Y G T Y G
>>>>>>>>>>>>>>>>>>exon 4>>>>>>>>>>>>>>>>>
>>>>>>>>>>>exon 3>>>>>>>>>>>
181 GCCCACTGAT GTCAGCTATA CCCAGGCTCA GACCACTGCA ACCTATGGGC AGACCGCCTA
Q P T D V S Y T Q A Q T T A T Y G Q T A
>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 4>>>>>>>>>>>>>>>>>>>>>>>>>>>>
241 TGCAACTTCT TATGGACAGC CTCCCACTGG TTATACTACT CCAACTGCCC CCCAGGCATA
Y A T S Y G Q P P T G Y T T P T A P Q A
>>>>>>>>>>>>>>>>exon 5>>>>>>>>>>>>>>>>
>>>>>>>>>>>>>exon 4>>>>>>>>>>>>>
301 CAGCCAGCCT GTCCAGGGGT ATGGCACTGG TGCTTATGAT ACCACCACTG CTACAGTCAC
Y S Q P V Q G Y G T G A Y D T T T A T V
>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 5>>>>>>>>>>>>>>>>>>>>>>>>>>>>
361 CACCACCCAG GCCTCCTATG CAGCTCAGTC TGCATATGGC ACTCAGCCTG CTTATCCAGC
T T T Q A S Y A A Q S A Y G T Q P A Y P
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 5>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
421 CTATGGGCAG CAGCCAGCAG CCACTGCACC TACAAGACCG CAGGATGGAA ACAAGCCCAC
A Y G Q Q P A A T A P T R P Q D G N K P
>>>>>>>>>>>exon 6>>>>>>>>>>>
>>>>>>>>>>>>>>>>>exon 5>>>>>>>>>>>>>>>>>
481 TGAGACTAGT CAACCTCAAT CTAGCACAGG GGGTTACAAC CAGCCCAGCC TAGGATATGG
T E T S Q P Q S S T G G Y N Q P S L G Y
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 6>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
541 ACAGAGTAAC TACAGTTATC CCCAGGTACC TGGGAGCTAC CCCATGCAGC CAGTCACTGC
G Q S N Y S Y P Q V P G S Y P M Q P V T
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 6>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

```
601  ACCTCCATCC TACCCTCCTA CCAGCTATTC CTCTACACAG CCGACTAGTT ATGATCAGAG
       A  P  P  S  Y  P  P  T  S  Y  S  S  T  Q  P  T  S  Y  D  Q
                                  >>>>>>>>>>>>>>>>>exon 7>>>>>>>>>>>>>>>
     >>>>>>>>>exon 6>>>>>>>>>>

661  CAGTTACTCT CAGCAGAACA CCTATGGGCA ACCGAGCAGC TATGGACAGC AGAGTAGCTA
       S  S  Y  S  Q  Q  N  T  Y  G  Q  P  S  S  Y  G  Q  Q  S  S
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 7>>>>>>>>>>>>>>>>>>>>>>>>>>>>

721  TGGTCAACAA AGCAGCTATG GGCAGCAGCC TCCCACTAGT TACCCACCCC AAACTGGATC
       Y  G  Q  Q  S  S  Y  G  Q  Q  P  P  T  S  Y  P  P  Q  T  G
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 7>>>>>>>>>>>>>>>>>>>>>>>>>>>>

781  CTACAGCCAA GCTCCAAGTC AATATAGCCA ACAGAGCAGC AGCTACGGGC AGCAGAGTTC
       S  Y  S  Q  A  P  S  Q  Y  S  Q  Q  S  S  S  Y  G  Q  Q  S
                                                                >>>>
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 7>>>>>>>>>>>>>>>>>>>>>>>>>>>>

841  ATTCCGACAG GACCACCCCA GTAGCATGGG TGTTTATGGG CAGGAGTCTG GAGGATTTTC
       S  F  R  Q  D  H  P  S  S  M  G  V  Y  G  Q  E  S  G  G  F
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 8>>>>>>>>>>>>>>>>>>>>>>>>>>>>

901  CGGACCAGGA GAGAACCGGA GCATGAGTGG CCCTGATAAC CGGGGCAGGG GAAGAGGGGG
       S  G  P  G  E  N  R  S  M  S  G  P  D  N  R  G  R  G  R  G
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 8>>>>>>>>>>>>>>>>>>>>>>>>>>>>

961  ATTTGATCGT GGAGGCATGA GCAGAGGTGG GCGGGGAGGA GGACGCGGTG GAATGGGCAG
       G  F  D  R  G  G  M  S  R  G  G  R  G  G  G  R  G  G  M  G
                                                                >>>
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 8>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1021 CGCTGGAGAG CGAGGTGGCT TCAATAAGCC TGGTGGACCC ATGGATGAAG GACCAGATCT
       S  A  G  E  R  G  G  F  N  K  P  G  G  P  M  D  E  G  P  D
                                        >>>>>>>>>>>exon 10>>>>>>>>>
     >>>>>>>>>>>>>>>>exon 9>>>>>>>>>>>>>>>>>

1081 TGATCTAGGC CCACCTGTAG ATCCAGATGA AGACTCTGAC AACAGTGCAA TTTATGTACA
       L  D  L  G  P  P  V  D  P  D  E  D  S  D  N  S  A  I  Y  V
              >>>>>>>>>>>>>>>>>>>>>>>>>>exon 11>>>>>>>>>>>>>>>>>>>>>>>>
     >>>>>>>>

1141 AGGATTAAAT GACAGTGTGA CTCTAGATGA TCTGGCAGAC TTCTTTAAGC AGTGTGGGGT
       Q  G  L  N  D  S  V  T  L  D  D  L  A  D  F  F  K  Q  C  G
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 11>>>>>>>>>>>>>>>>>>>>>>>>>>>>
```

```
1201  TGTTAAGATG AACAAGAGAA CTGGGCAACC CATGATCCAC ATCTACCTGG ACAAGGAAAC
      V  V  K  M   N  K  R   T  G  Q   P  M  I  H   I  Y  L   D  K  E
            >>>>>>>>>>>>>>>>>>>>>>>>>>>exon 12>>>>>>>>>>>>>>>>>>>>>>>>
      >>>>>>>

1261  AGGAAAGCCC AAAGGCGATG CCACAGTGTC CTATGAAGAC CCACCCACTG CCAAGGCTGC
      T  G  K  P   K  G  D   A  T  V   S  Y  E  D   P  P  T   A  K  A
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 12>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1321  CGTGGAATGG TTTGATGGGA AAGATTTTCA AGGGAGCAAA CTTAAAGTCT CCCTTGCTCG
      A  V  E  W   F  D  G   K  D  F   Q  G  S  K   L  K  V   S  L  A
                        >>>>>>>>>>>>>>>>>>>>exon 13>>>>>>>>>>>>>>>>>>>>
      >>>>>exon 12>>>>>>

1381  GAAGAAGCCT CCAATGAACA GTATGCGGGG TGGTCTGCCA CCCCGTGAGG GCAGAGGCAT
      R  K  K  P   P  M  N   S  M  R   G  G  L  P   P  R  E   G  R  G
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 13>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1441  GCCACCACCA CTCCGTGGAG GTCCAGGAGG CCCAGGAGGT CCTGGGGGAC CCATGGGTCG
      M  P  P  P   L  R  G   G  P  G   G  P  G  G   P  G  G   P  M  G
                           >>>>>>>>>>>>>>>>>>>exon 14>>>>>>>>>>>>>>>>>>
      >>>>>>exon 13>>>>>>>>

1501  CATGGGAGGC CGTGGAGGAG ATAGAGGAGG CTTCCCTCCA AGAGGACCCC GGGGTTCCCG
      R  M  G  G   R  G  G   D  R  G   G  F  P  P   R  G  P   R  G  S
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 14>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1561  AGGGAACCCC TCTGGAGGAG GAAACGTCCA GCACCGAGCT GGAGACTGGC AGTGTCCCAA
      R  G  N  P   S  G  G   G  N  V   Q  H  R  A   G  D  W   Q  C  P
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 14>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1621  TCCGGGTTGT GGAAACCAGA ACTTCGCCTG GAGAACAGAG TGCAACCAGT GTAAGGCCCC
      N  P  G  C   G  N  Q   N  F  A   W  R  T  E   C  N  Q   C  K  A
         >>>>>>>>>>>>>>>>exon 15b>>>>>>>>>>>>>>>>>>>>>>>>>>>
         >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 15>>>>>>>>>>>>>>>>>>>>>>>>
      >>>

1681  AAAGCCTGAA GGCTTCCTCC CGCCACCCTT TCCGCCCCCG GGTGGTGATC GTGGCAGAGG
      P  K  P  E   G  F  L   P  P  P   F  P  P  P   G  G  D   R  G  R
                                                        >>>>>>>exon 16>>>>>>
      >>>>>>>>>>>>>>>>>>>exon 15>>>>>>>>>>>>>>>>>>>>
```

```
1741  TGGCCCTGGT GGCATGCGGG GAGGAAGAGG TGGCCTCATG GATCGTGGTG GTCCCGGTGG
      G  G  P  G   G  M  R   G   G  R   G  G  L  M   D  R  G   G  P  G
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 16>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1801  AATGTTCAGA GGTGGCCGTG GTGGAGACAG AGGTGGCTTC CGTGGTGGCC GGGGCATGGA
      G  M  F  R   G  G  R   G   G  D   R  G  G  F   R  G  G   R  G  M
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 16>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1861  CCGAGGTGGC TTTGGTGGAG GAAGACGAGG TGGCCCTGGG GGGCCCCCTG GACCTTTGAT
      D  R  G  G   F  G  G   G  R  R   G  G  P  G   G  P  P   G  P  L
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 16>>>>>>>>>>>>>>>>>>>>>>>>>>>>

1921  GGAACAGATG GGAGGAAGAA GAGGAGGACG TGGAGGACCT GGAAAAATGG ATAAAGGCGA
      M  E  Q  M   G  G  R   R  G  G   R  G  G  P   G  K  M   D  K  G
                                                                >>>>>>
      >>>>>>>>>>>>>>>>>>>>>>>>>>>exon 16>>>>>>>>>>>>>>>>>>>>>>>>>>

1981  GCACCGTCAG GAGCGCAGAG ATCGGCCCTA Ctagatgcag agaccccgca gagctgcatt
      E  H  R  Q   E  R  R   D  R  P   Y  stop
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>>>>>>>>>>>>>>

2041  gactaccaga tttatttttt aaaccagaaa atgttttaaa tttataattc catatttata
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>>>>>>>>>>>>>>

2101  atgttggcca caacattatg attattcctt gtctgtactt tagtattttt caccatttgt
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>>>>>>>>>>>>>>

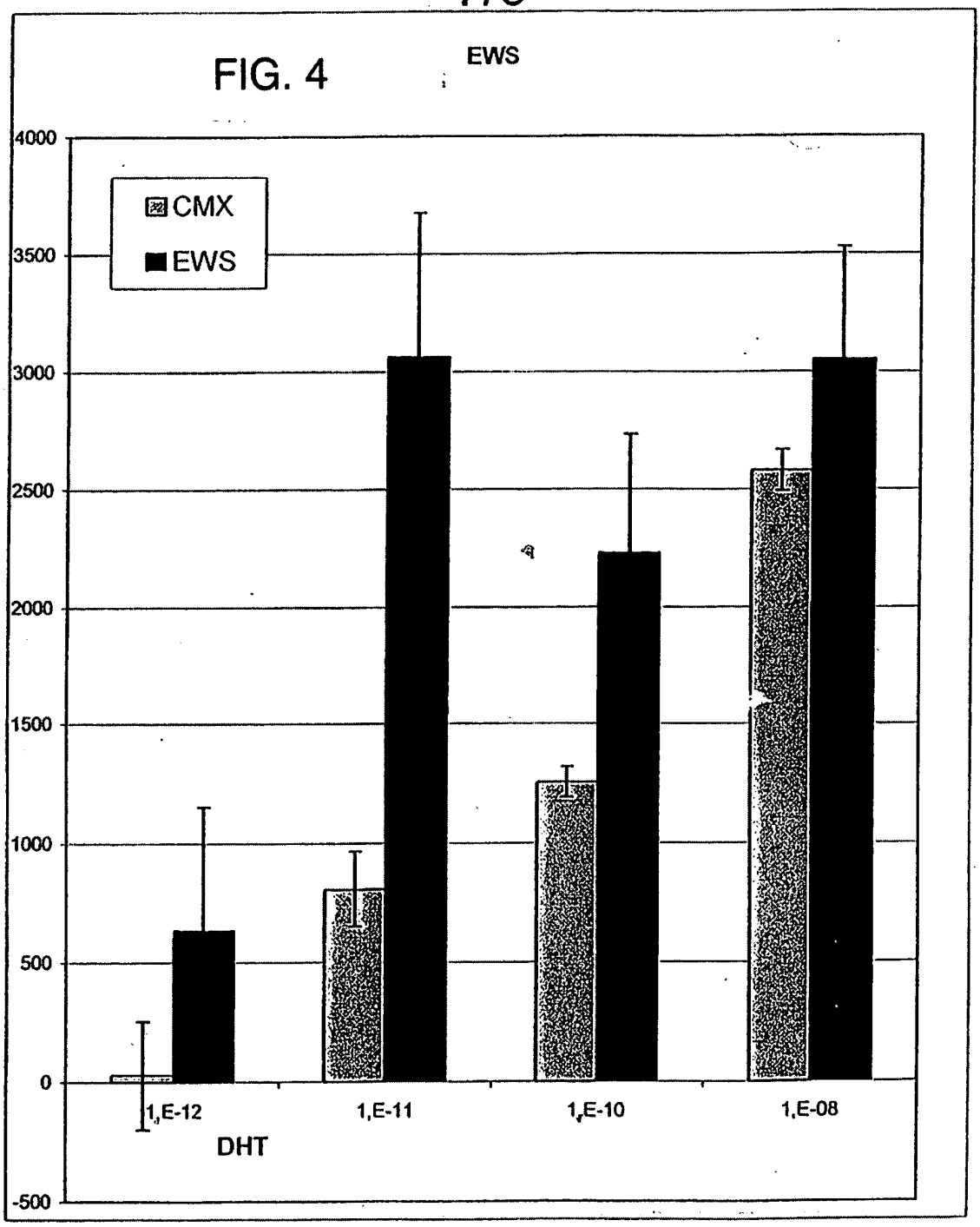
2161  gaagaaacat taaaacaagt taaatggtag tgtgcggagt ttttttttct tccttctttt
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>>>>>>>>>>>>>>

2221  aaaaatggtt gtttaagact ttaacaatgg gaaccccttg tgagcatgct cagtatcatt
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>>>>>>>>>>>>>>

2281  gtggagaacc aagagggcct cttaactgta acaatgttca tggttgtgat gttttttttt
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>>>>>>>>>>>>>>

2341  ttttttttaaa ataaaattcc aaatgtttaa taaaaaaaaa aaaaaaaaaa
      >>>>>>>>>>>>>>exon 17>>>>>>>>>>>>>>>
```

FIG. 4


EWS
CMX
EWS
4000
3500
3000
2500
2000
1500
1000
500
0
-500
1,E-12
1,E-11
1,E-10
1,E-08
DHT

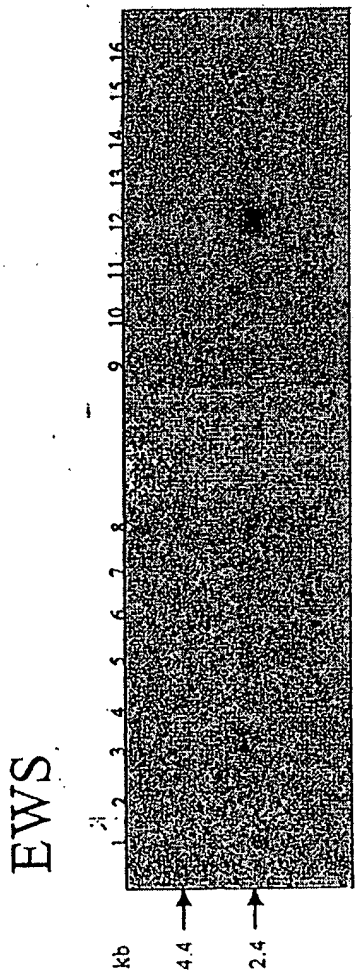
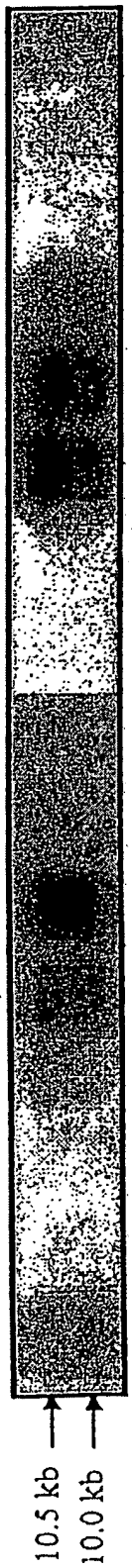

EWS
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
kb
4.4
2.4

FIG. 5a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10.5 kb
10.0 kb

FIG. 5b

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Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln Gly Tyr Ser Ala
5 10 15 20

tac acc gcc cag ccc act caa gga tat gca cag acc acc cag gca tat 151
Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr Thr Gln Ala Tyr
25 30 35

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Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr Asp Val Ser Tyr
40 45 50

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Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr Ala Tyr Ala Thr
55 60 65

tct tat gga cag cct ccc act ggt tat act act cca act gcc ccc cag 295
Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro Thr Ala Pro Gln
70 75 80

gca tac agc cag cct gtc cag ggg tat ggc act ggt gct tat gat acc 343
Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly Ala Tyr Asp Thr
85 90 95 100

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acc act gct aca gtc acc acc acc cag gcc tcc tat gca gct cag tct   391
Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr Ala Ala Gln Ser
                105                 110                 115

gca tat ggc act cag cct gct tat cca gcc tat ggg cag cag cca gca   439
Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly Gln Gln Pro Ala
            120                 125                 130

gcc act gca cct aca aga ccg cag gat gga aac aag ccc act gag act   487
Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys Pro Thr Glu Thr
        135                 140                 145

agt caa cct caa tct agc aca ggg ggt tac aac cag ccc agc cta gga   535
Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln Pro Ser Leu Gly
    150                 155                 160

tat gga cag agt aac tac agt tat ccc cag gta cct ggg agc tac ccc   583
Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro Gly Ser Tyr Pro
165                 170                 175                 180

atg cag cca gtc act gca cct cca tcc tac cct cct acc agc tat tcc   631
Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro Thr Ser Tyr Ser
                185                 190                 195

tct aca cag ccg act agt tat gat cag agc agt tac tct cag cag aac   679
Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr Ser Gln Gln Asn
            200                 205                 210

acc tat ggg caa ccg agc agc tat gga cag cag agt agc tat ggt caa   727
Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln
        215                 220                 225

caa agc agc tat ggg cag cag cct ccc act agt tac cca ccc caa act   775
Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr Pro Pro Gln Thr
    230                 235                 240

gga tcc tac agc caa gct cca agt caa tat agc caa cag agc agc agc   823
Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln Ser Ser Ser
245                 250                 255                 260

tac ggg cag cag agt tca ttc cga cag gac cac ccc agt agc atg ggt   871
Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro Ser Ser Met Gly
                265                 270                 275

gtt tat ggg cag gag tct gga gga ttt tcc gga cca gga gag aac cgg   919
Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro Gly Glu Asn Arg
            280                 285                 290

agc atg agt ggc cct gat aac cgg ggc agg gga aga ggg gga ttt gat   967
Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg Gly Gly Phe Asp
        295                 300                 305

cgt gga ggc atg agc aga ggt ggg cgg gga gga gga cgc ggt gga atg   1015
Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly Arg Gly Gly Met
    310                 315                 320
```

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ggc agc gct gga gag cga ggt ggc ttc aat aag cct ggt gga ccc atg   1063
Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly Gly Pro Met
325                 330                 335                 340

gat gaa gga cca gat ctt gat cta ggc cca cct gta gat cca gat gaa   1111
Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val Asp Pro Asp Glu
                345                 350                 355

gac tct gac aac agt gca att tat gta caa gga tta aat gac agt gtg   1159
Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn Asp Ser Val
            360                 365                 370

act cta gat gat ctg gca gac ttc ttt aag cag tgt ggg gtt gtt aag   1207
Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly Val Val Lys
        375                 380                 385

atg aac aag aga act ggg caa ccc atg atc cac atc tac ctg gac aag   1255
Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr Leu Asp Lys
    390                 395                 400

gaa aca gga aag ccc aaa ggc gat gcc aca gtg tcc tat gaa gac cca   1303
Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr Glu Asp Pro
405                 410                 415                 420

ccc act gcc aag gct gcc gtg gaa tgg ttt gat ggg aaa gat ttt caa   1351
Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys Asp Phe Gln
                425                 430                 435

ggg agc aaa ctt aaa gtc tcc ctt gct cgg aag aag cct cca atg aac   1399
Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro Pro Met Asn
            440                 445                 450

agt atg cgg ggt ggt ctg cca ccc cgt gag ggc aga ggc atg cca cca   1447
Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg Gly Met Pro Pro
        455                 460                 465

cca ctc cgt gga ggt cca gga ggc cca gga ggt cct ggg gga ccc atg   1495

Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Met
    470                 475                 480

ggt cgc atg gga ggc cgt gga gga gat aga gga ggc ttc cct cca aga   1543
Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe Pro Pro Arg
485                 490                 495                 500

gga ccc cgg ggt tcc cga ggg aac ccc tct gga gga gga aac gtc cag   1591
Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Gly Asn Val Gln
                505                 510                 515

cac cga gct gga gac tgg cag tgt ccc aat ccg ggt tgt gga aac cag   1639
His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys Gly Asn Gln
            520                 525                 530

aac ttc gcc tgg aga aca gag tgc aac cag tgt aag gcc cca aag cct   1687
Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro
        535                 540                 545
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Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly
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Gln Gln Pro Ala Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys
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Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro
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210 215 220

Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr
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Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln
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355 360 365

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370 375 380

Gly Val Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile
385 390 395 400

Tyr Leu Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser
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Tyr Glu Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly
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Lys Asp Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys
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Pro Pro Met Asn Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg
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Gly Met Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro
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Gly Gly Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly
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Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
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Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly
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Cys Gly Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys
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Ala Pro Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly
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Gly Asp Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly
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Gly Leu Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg
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Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly
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Gly Phe Gly Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro
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Leu Met Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly
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Lys Met Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
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